


```

COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US7097669, 31005
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 415
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/94 and 3/6/94; PCT/JP94/17007
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
RELIGATION NUMBER: 27101
REFERENCE/Docket NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3252
TELEFAX: (212)953-3252
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
POPOLNRY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT FEESTERS IN SEQ ID NO: 20
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-09-568-3100-20

Query Match: 67.9%; Score 320; Dh 27; Length 92;
Best Local Similarity: 68.1%; Pos: No. 6, Le-33;
Matches: 62; Conservative: 10; Mismatches: 30; Gaps: 0;

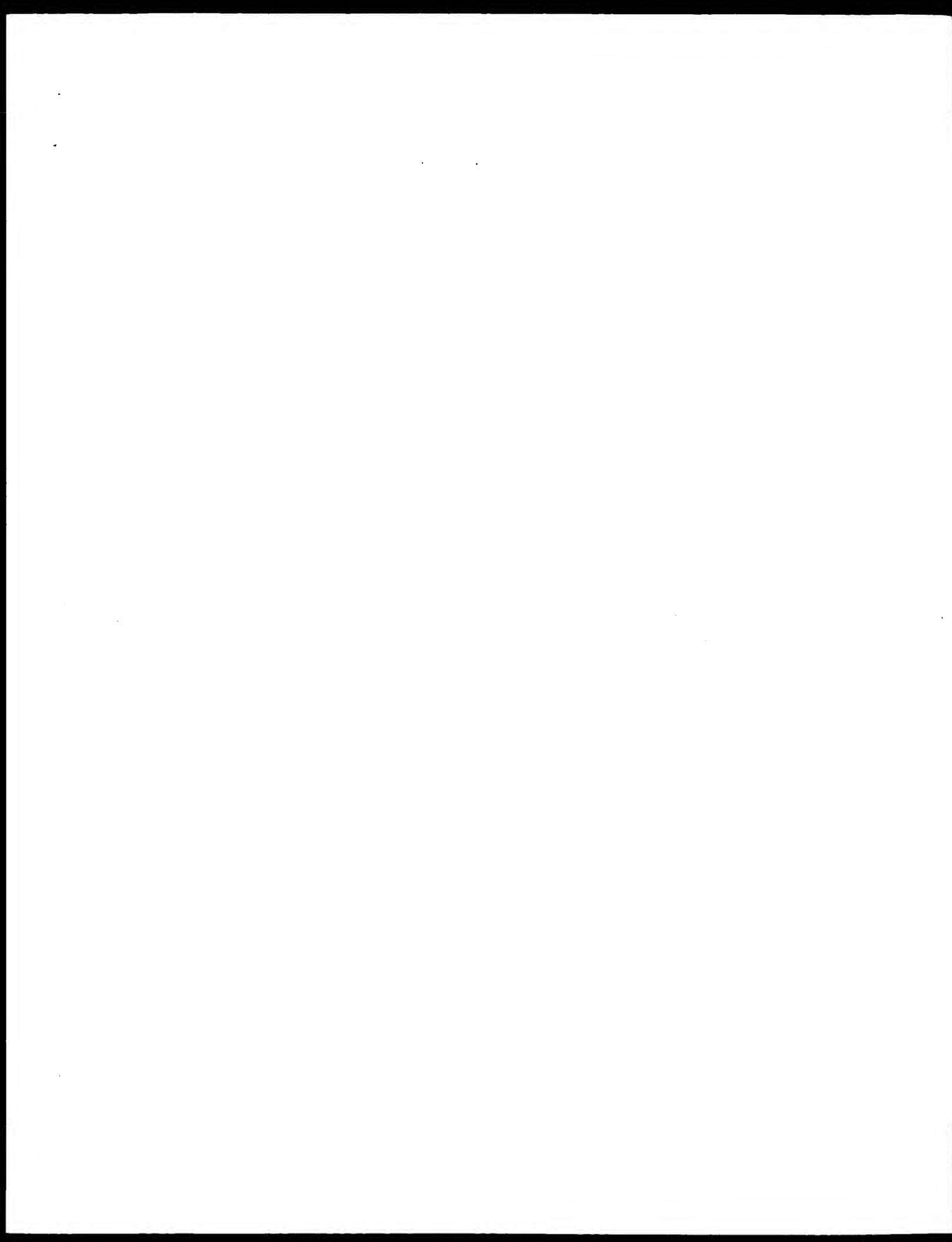
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D6 2 IKELHELVIVHFFITVFSSVSEFTTSKTFSLRLFLAKLNLGNTFAVTHFEGL 61
QY 61 IANGQVEFKREVLTVDLTADNHIRE 91
D6 62 IANGQVDPDPTFTSISVALVAAYRHHRE 92

RESULT 5
US-09-270-455-20
Sequence 20: Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TORUJIRO
APPLICANT: KIMURA, TATSUHI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: WYATT,GERHAR,MILLER & ASSOCIATES
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE:
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 415
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/568,310

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[illegible]

[illegible]




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FILE REFERENCE: RCT
CURRENT AWARD: 2002-03-14
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent V. 2.1
SEQ ID NO: 2
LENGTH: 101
TYPE: PRT
ORGANISM: Mus musculus
US-09-646-651a-2

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Query Match
Best Local Similarity: 36.98; Pct. No. 1.66-100
Matches: 31; Conservative: 22; Mismatches: 31; Indels: 0; Gaps: 0

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QY 3 LEAD/INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
DQ 5 LEAD/INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
QY 63 NEUROGENIC COMPOSITIONS AND METHODS
DQ 65 NEUROGENIC COMPOSITIONS AND METHODS

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RESULT 14
US-09-781-509-2
Sequence 2, Application US/09781509
Patent No. US20020099010A1
GENERAL INFORMATION:
APPLICANT: Lukand, Eugene
APPLICANT: Bock, Elisabeth M.
APPLICANT: Berezov, Vladimir
TITLE OF INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: RCT
CURRENT APPLICATION NUMBER: US/09781 509
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 09/7393 433
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent V. 2.1
SEQ ID NO: 2
LENGTH: 101
TYPE: PRT
ORGANISM: Mus musculus
US-09-781-509-2

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Query Match
Best Local Similarity: 36.98; Pct. No. 1.66-100
Matches: 31; Conservative: 22; Mismatches: 31; Indels: 0; Gaps: 0

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QY 3 LEAD/INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
DQ 5 LEAD/INVENTION: NEUROGENIC COMPOSITIONS AND METHODS
QY 63 NEUROGENIC COMPOSITIONS AND METHODS
DQ 65 NEUROGENIC COMPOSITIONS AND METHODS

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RESULT 15
US-10-097-340-270
Sequence 270, Application US/10097340
Patent No. US20040087250A1
GENERAL INFORMATION:
APPLICANT: John Monahan
APPLICANT: Manjula Kannanavaram
APPLICANT: Sebastian Hiersch
APPLICANT: Shubhangi Kamarkar
APPLICANT: Steve G. Kovats
APPLICANT: Karel E. Meyers
APPLICANT: Michael Morrissey
APPLICANT: Peter Olandi
APPLICANT: Ami Sen

```

```

APPLICANT: Peter Velny
APPLICANT: Robert E. Mills
APPLICANT: Robert C. Bast, Jr.
APPLICANT: Karen Lu
APPLICANT: Rosemarie Schmandt
APPLICANT: Xunlei Zhao
APPLICANT: Karen Glatt
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins for the Identification,
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/425,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/424,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/411,742
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/725,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/723,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 964
SOFTWARE: FastSB for Windows Version 4.0
SEQ ID NO: 270
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-270

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Query Match
Best Local Similarity: 42.58; Pct. No. 9; Length 94;
Matches: 34; Conservative: 19; Mismatches: 35; Indels: 0; Gaps: 0

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QY 1 LEAD/INVENTION: Nucleic Acid Molecules and Proteins for the Identification,
DQ 2 LEAD/INVENTION: Nucleic Acid Molecules and Proteins for the Identification,
QY 61 NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION,
DQ 63 NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION,

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Query Match
Best Local Similarity: 42.58; Pct. No. 9; Length 94;
Matches: 34; Conservative: 19; Mismatches: 35; Indels: 0; Gaps: 0

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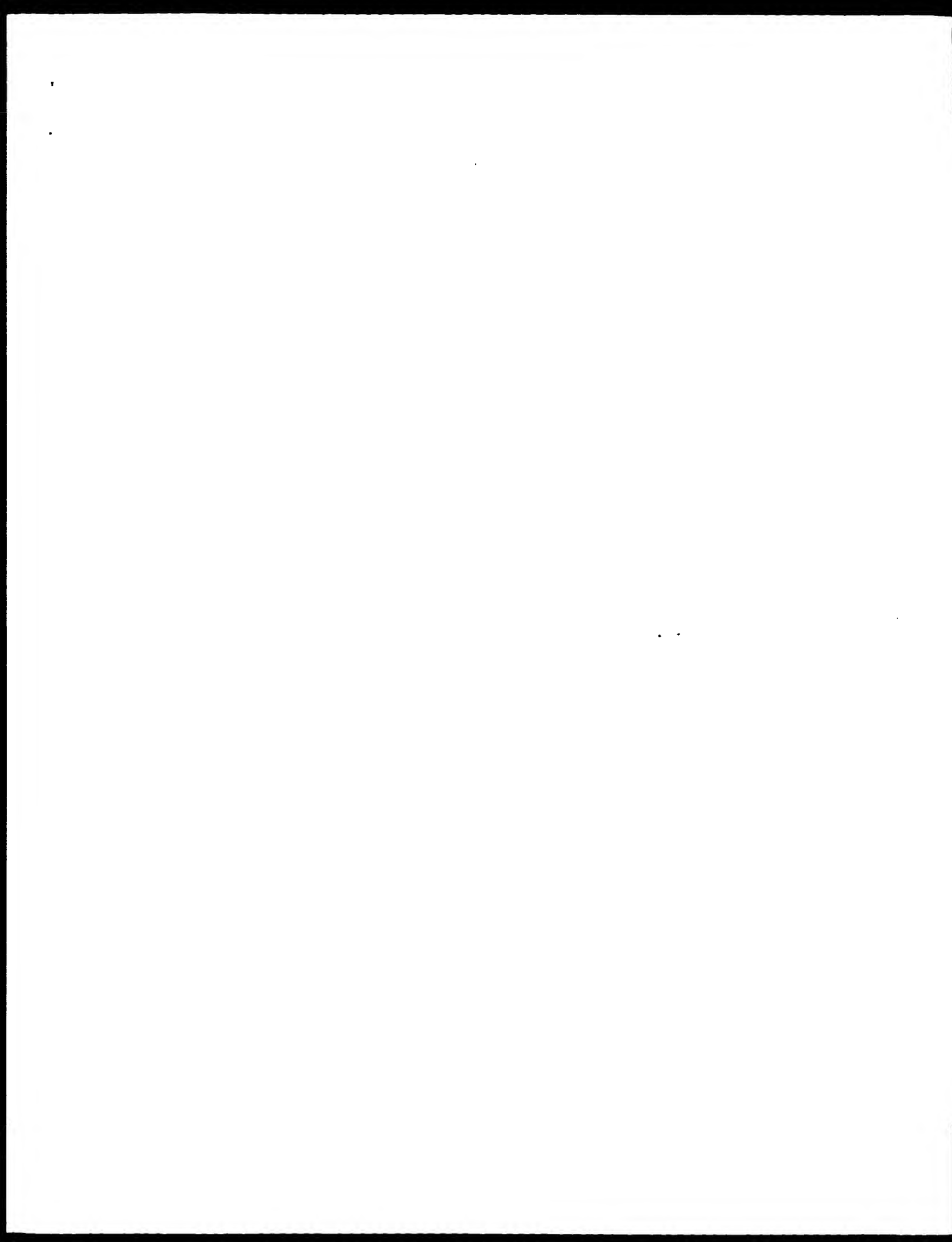
QY 1 LEAD/INVENTION: Nucleic Acid Molecules and Proteins for the Identification,
DQ 2 LEAD/INVENTION: Nucleic Acid Molecules and Proteins for the Identification,
QY 61 NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION,
DQ 63 NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION,

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Query Match
Best Local Similarity: 42.58; Pct. No. 9; Length 94;
Matches: 34; Conservative: 19; Mismatches: 35; Indels: 0; Gaps: 0

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GenCore version 5.1.4-PL4778
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OM protein - protein search, using sw model

Run on: May 15, 2003, 11:44:19 : Search time 322 seconds

(without alignment)

176.21 kDa, 176.21 kDa, 176.21 kDa

Title: US-09-646-651A-1

Sequence: 1 TRPMMPTMIFRCSVP

Scoring table: BLASTM62

Gap: 10.0, Expect 0.5

Search: 456014 seqs, 64433110 residues

Total number of hits satisfying chosen parameters: 456014

Minimum DB seq length: 9

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database	Accession	Score	Length	Expect	Description
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5	US-09-646-651A-1	471	100.0	0.5	US-09-646-651A-1
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14	US-09-646-651A-1	471	100.0	0.5	US-09-646-651A-1
15	US-09-646-651A-1	471	100.0	0.5	US-09-646-651A-1
16	US-09-646-651A-1	471	100.0	0.5	US-09-646-651A-1
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	455	96.6	US-09-646-651A-1	US-09-646-651A-1
5	443	94.1	US-09-646-651A-1	US-09-646-651A-1
6	359	76.3	US-09-646-651A-1	US-09-646-651A-1

7	354	75.2	US-09-646-651A-1	US-09-646-651A-1
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17	354	75.2	US-09-646-651A-1	US-09-646-651A-1
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19	354	75.2	US-09-646-651A-1	US-09-646-651A-1
20	354	75.2	US-09-646-651A-1	US-09-646-651A-1
21	354	75.2	US-09-646-651A-1	US-09-646-651A-1
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44	354	75.2	US-09-646-651A-1	US-09-646-651A-1
45	354	75.2	US-09-646-651A-1	US-09-646-651A-1

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4	US-09-646-651A-1	455	96.6	0.5	US-09-646-651A-1
5	US-09-646-651A-1	443	94.1	0.5	US-09-646-651A-1
6	US-09-646-651A-1	359	76.3	0.5	US-09-646-651A-1
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21	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
22	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
23	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
24	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
25	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
26	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
27	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
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29	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
30	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
31	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
32	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
33	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
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43	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1
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45	US-09-646-651A-1	354	75.2	0.5	US-09-646-651A-1

Sequence 9: Application US/08761285

GENERAL INFORMATION:

APPLICANT: NI, J., ET AL.

TITLE OF INVENTION: Human Chemotactic Cytokine 1

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARCELLA, HENRI, RAIN, GUILLIAN.

STREET: 6 BROOK FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761 285

FILING DATE: December 6, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/090897

FILING DATE: December 8, 1995

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DECKET NUMBER: 325809-505 (P410)

TELEPHONE: 201-994-1709

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 91 AMINO ACIDS

TYPE: AMINO ACID

STRANDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

US-08-761-285-9

Query Match 94.1% Score 443 DB 11 Length 91

Best Local Similarity 95.6% Prod. No. 6,700-443

Matches 87 Conservative 1 Mismatches 3 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91

HE 1 TLFEEHFIINFEVSVPLVLTIVLITAHNDHKE 91

DB 61 DANODEVSKFEVVLVITVITAHNDHKE 91

DB 61 NANODEVSKFEVVLVITVITAHNDHKE 91

RESULT 6

US-09-791-537-001P

Sequence 6: Application US/09/791 537

GENERAL INFORMATION:

APPLICANT: Biotechnology, Inc.

APPLICANT: Devec, Derek

APPLICANT: Dancer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUC-20815 OF PROTEIN FAMILIES AND FAMILY MEMB

FILE REFERENCE: 241/210

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 15055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 99618

LENGTH: 92

TYPE: PRT

ORGANISM: B. Taurus

US-09-791-537-99618

Query Match 75.2% Score 454 DB 16 Length 90

Best Local Similarity 78.9% Prod. No. 200-433

Matches 71 Conservative 9 Mismatches 10 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91

HE 1 TLFEEHFIINFEVSVPLVLTIVLITAHNDHKE 91

DB 61 DANODEVSKFEVVLVITVITAHNDHKE 91

DB 61 NANODEVSKFEVVLVITVITAHNDHKE 91

Query Match 76.2% Score 359 DB 21 Length 92

Best Local Similarity 79.1% Prod. No. 5,40-443

Matches 72 Conservative 9 Mismatches 10 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91

HE 1 TLFEEHFIINFEVSVPLVLTIVLITAHNDHKE 91

DB 61 DANODEVSKFEVVLVITVITAHNDHKE 91

DB 61 NANODEVSKFEVVLVITVITAHNDHKE 91

RESULT 7

US-09-167-705-3

Sequence 3: Application US/09167705B

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie

APPLICANT: Scott, David

TITLE OF INVENTION: Enzyme-Linked Receptor Binding Protein (EBR) and

FILE REFERENCE: 0576/5273

CURRENT FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 90

TYPE: PRT

ORGANISM: Human

US-09-167-705-3

Query Match 75.2% Score 354 DB 15 Length 90

Best Local Similarity 78.9% Prod. No. 200-433

Matches 71 Conservative 9 Mismatches 10 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91

HE 1 TLFEEHFIINFEVSVPLVLTIVLITAHNDHKE 91

DB 61 DANODEVSKFEVVLVITVITAHNDHKE 91

DB 61 NANODEVSKFEVVLVITVITAHNDHKE 91

RESULT 8

US-09-263-312-3

Sequence 3: Application US/09263312

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie

APPLICANT: Scott, David

TITLE OF INVENTION: Enzyme-Linked Receptor Binding Protein (EBR) and

FILE REFERENCE: 0576/5273 A

CURRENT FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 90

TYPE: PRT

ORGANISM: Human

US-09-263-312-3

Query Match 75.2% Score 354 DB 16 Length 90

Best Local Similarity 78.9% Prod. No. 200-433

Matches 71 Conservative 9 Mismatches 10 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91

HE 1 TLFEEHFIINFEVSVPLVLTIVLITAHNDHKE 91

DB 61 DANODEVSKFEVVLVITVITAHNDHKE 91

DB 61 NANODEVSKFEVVLVITVITAHNDHKE 91

RESULT 9

US-09-263-312-3

Sequence 3: Application US/09263312

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie

APPLICANT: Scott, David

TITLE OF INVENTION: Enzyme-Linked Receptor Binding Protein (EBR) and

FILE REFERENCE: 0576/5273 A

CURRENT FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 5

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SEQ ID NO 3

LENGTH: 90

TYPE: PRT

ORGANISM: Human

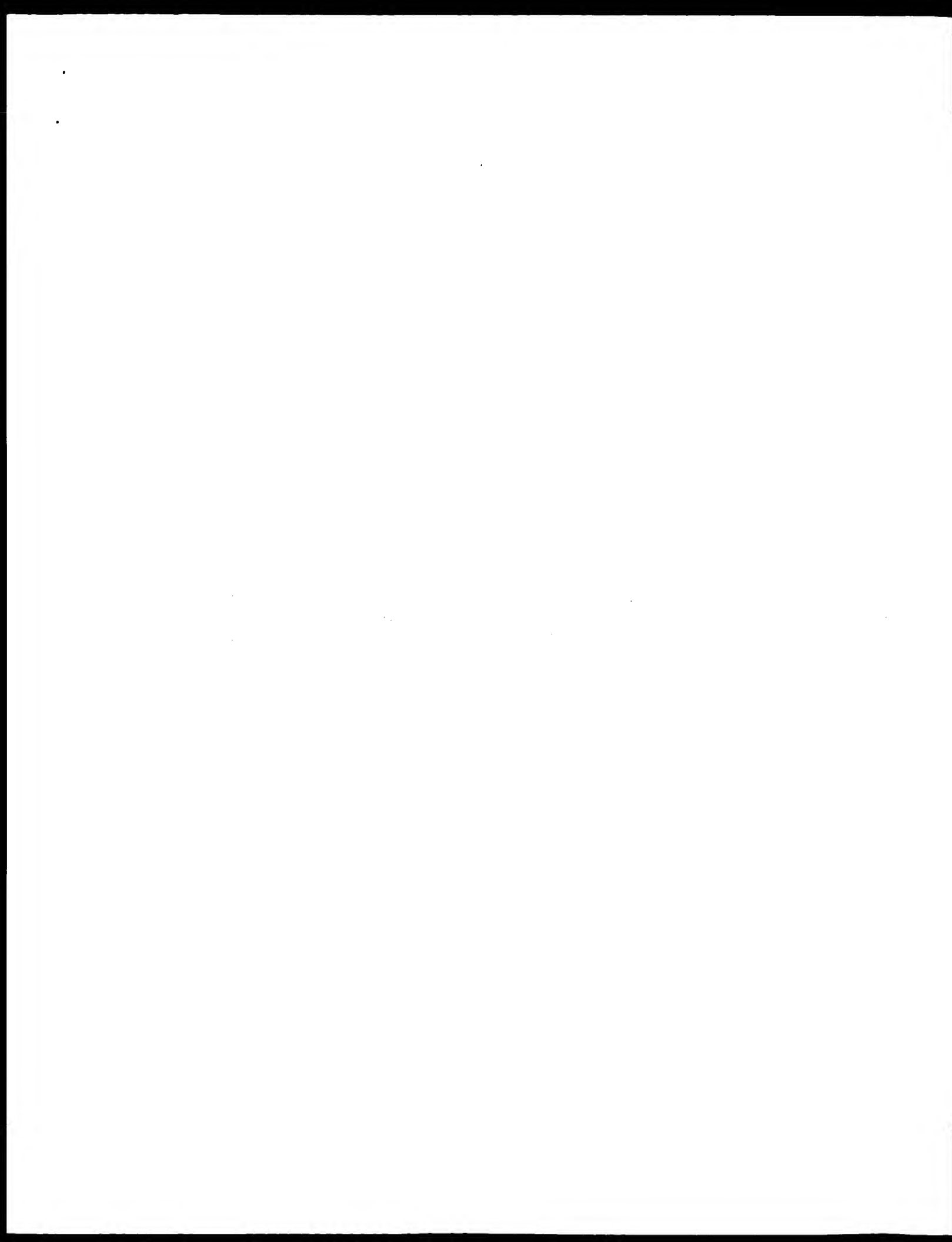
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Query Match 75.2% Score 354 DB 16 Length 90

Best Local Similarity 78.9% Prod. No. 200-433

Matches 71 Conservative 9 Mismatches 10 Indels 0 Caps 0

QY 1 FILE:HEBENININFEVSVPLVLTIVLITAHNDHKE 91



db 62 LITNARKSTEFIMMARIWASHENKHE 92

RESULT 7

Best Local Similarity 45.1%, Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 0; Gaps 1;

GENERAL INFORMATION:
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
FILE REFERENCE: D0190 NP
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: 60/337,429
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patent In version 3.1
SEQ ID NO 32
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
PT-INS-2 3446; 42

Query Match 43.6%, Score 205.5; DB 6; Length 114;
Best Local Similarity 45.1%, Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 0; Gaps 1;

db 62 LITNARKSTEFIMMARIWASHENKHE 92

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db 62 LITNARKSTEFIMMARIWASHENKHE 92

APPLICANT: NADLER, STEVEN G.

APPLICANT: CARMAN, JOLIE

TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE

FILE REFERENCE: 3054-4191

CURRENT FILING DATE: 2003-01-14

NUMBER OF SEQ ID NOS: 746

SOFTWARE: Patent In ver. 2.1

SEQ ID NO 340

LENGTH: 114

TYPE: PRT

ORGANISM: Homo sapiens

US-09-646-651a-1.rapn

Query Match 43.6%, Score 205.5; DB 7; Length 114;
Best Local Similarity 45.1%, Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 0; Gaps 1;

db 62 LITNARKSTEFIMMARIWASHENKHE 92

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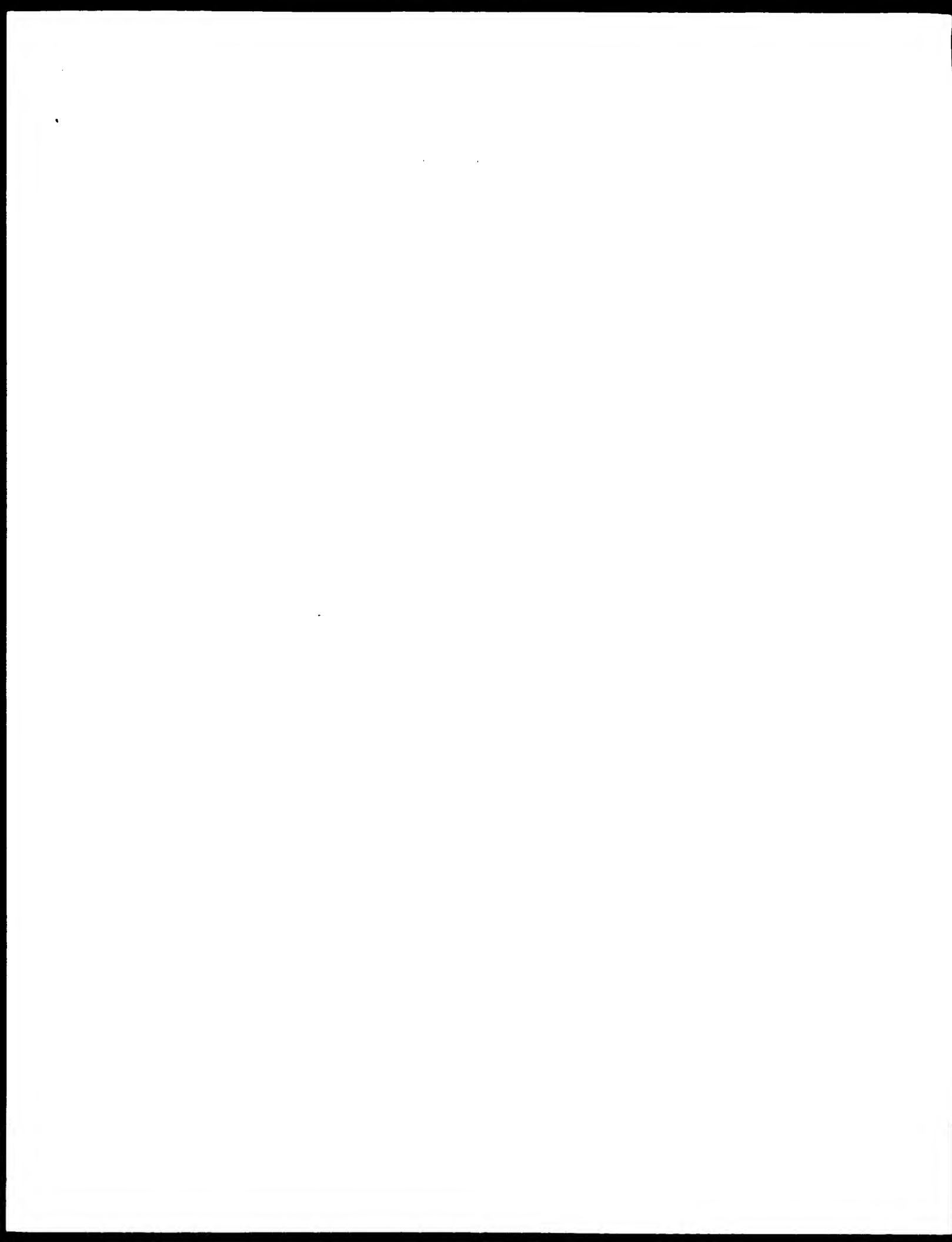
db 62 LITNARKSTEFIMMARIWASHENKHE 92

Thu May 15 11:47:29 2003

us-09-646-651a-1.rapn

Page 5

Search completed: May 15, 2003, 11:44:59
Job time : 90 secs



GenCode version 5.1.4_p5_4578
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OM protein - protein search, using ew model

Run on: May 15, 2003, 11:34:18 : Search time 17 seconds

(without alignment)
514,502 Million cell updates/sec

Title: US-09-646-651A-1

Perfect score: 471

Sequence: 1 IRTFMFPIINIFRYSV

EVVVEVVEVITAMNIKE 91

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 263224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 263224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 99

Listing first 45 summaries

Database:

1: PIR33*
2: PIR11*
3: PIR33*
4: PIR43*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	455	96.6	91	2	A55406
2	379	77.7	92	1	PIR112
3	251.5	53.4	122	1	A42628
4	207.5	43.6	114	1	B11848
5	196.5	41.7	113	1	JN0686
6	179	48.0	95	2	S-4146
7	168.5	45.8	113	1	S68242
8	163	44.6	95	1	S35985
9	157	44.3	89	1	156163
10	157	44.3	101	2	S06207
11	156	43.1	92	1	A26577
12	155	42.9	91	1	B61038
13	155	42.9	92	2	A48015
14	154	42.7	92	1	BCH018
15	154	42.7	94	1	Refc1A
16	154	42.7	101	2	S01759
17	154	42.7	89	1	990785
18	153	42.5	94	1	BCH01A
19	150	41.8	101	2	A48219
20	149	41.6	102	1	J01380
21	147	41.2	100	2	A53217
22	145	39.8	93	1	BCH03F
23	145	39.8	105	1	137680
24	144	39.6	591	2	A45145
25	143	39.4	98	2	A41988
26	140	39.7	307	2	A48118
27	136.5	29.0	110	1	B48219
28	134.5	29.6	79	1	JN0476
29	134.5	28.3	97	2	A28489

ALIGNMENTS

RESULT 1

A55406

calcitrinin C - pig

C-Specific: Sus scrofa domestica (domestic pig)

Database: 10 Feb 1995 480 proteins, 10 Feb 1995 #1 to change 27-May-1997

C66Accession: A55406

Kubell, Angolica, E.C., Schlotter, C.H., Santome, J.A.

J. Biol. Chem. 269, 28920-28946, 1994

Abstract: Primary structure and binding properties of calcitrinin C, a novel S100-like

Accession: A55406

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Keywords: acetylated amino acid, calcium binding, EF hand, bone, bone density, bone mineral density, calcium, calcium metabolism

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EF1: 4/1/99 abstract information in status produced: 06/01

EF3: 4/1/99 abstract information in status produced: 06/01

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Abstract: type: protein

C:Superfamily: S-100 proteins; calmodulin repeat homology

C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc

F:2-94/Protein: S-100 Protein alpha chain #status predicted (MA)

F:7-41/Domain: calmodulin repeat homology (EP)

F:50-82/Domain: calmodulin repeat homology (EP)

F:2/Modified sites: blocked amino end (Gly) (in mature form) (probably acetylated) #status predicted

F:20,23,25,29,33/Binding sites: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted

F:63,65,67,69,74/Binding sites: calcium (Asp, Asn, Asp, Glu, Glu) #status predicted

Query Match 32.78; Score 154; DB 1; Length 94;

Best local similarity 38.48; Pred. No. 4, 1e-08;

Matches 33; Conservative 18; Mismatches 35; Gaps 0;

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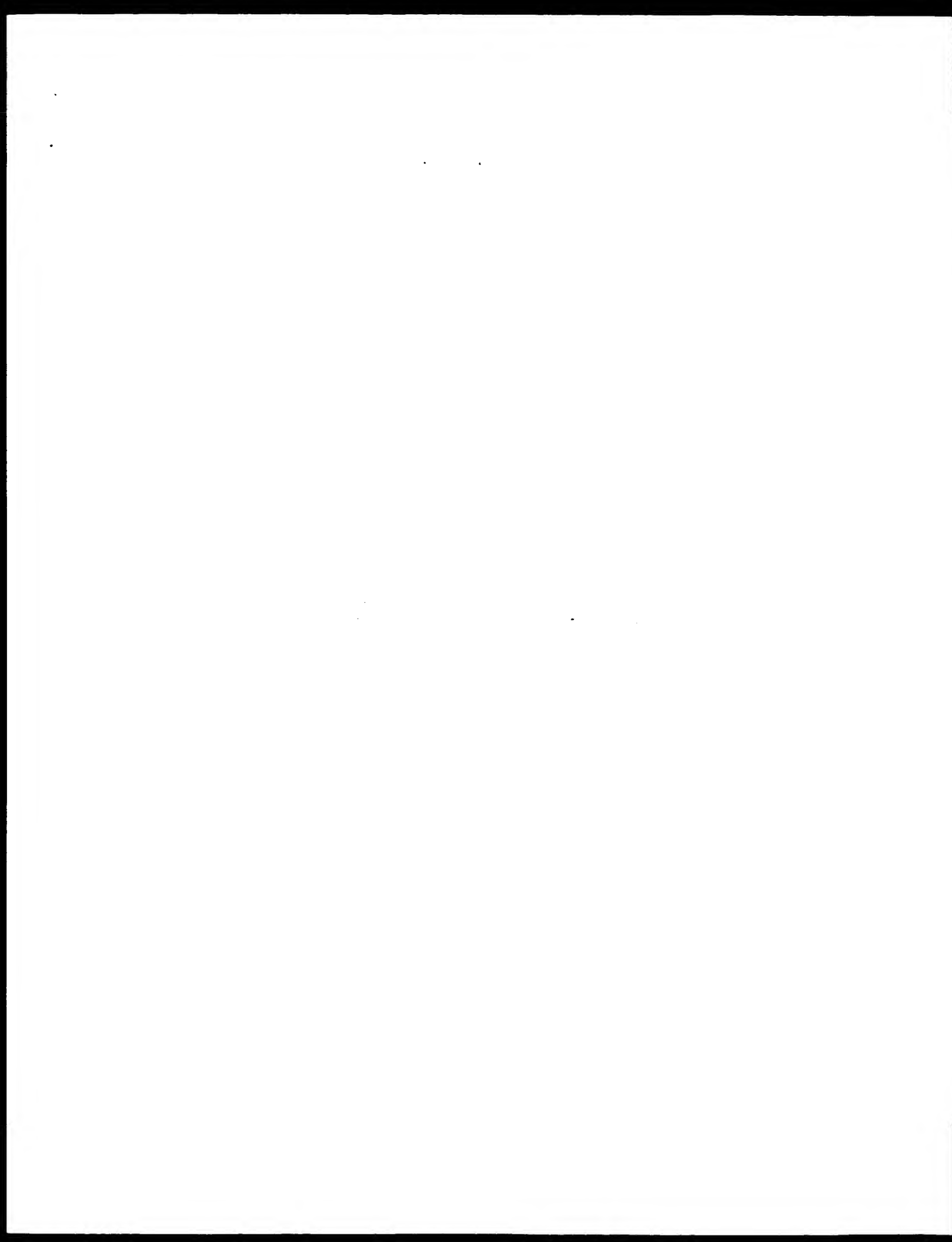
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QY 61 DAMDQVSPKEPVLVTDLLIAHD 86

DB 63 DDMQDQVLTQEVYVAALTVACNN 88

Search completed: May 15, 2003, 11:34:44

Job time : 18 secs



GenCore version 5.1.4_P5_4574
Copyright (c) 1993 - 2003 Computer Labs

OM protein - protein search, using SW model

Port 9000 May 15, 2003, 11:44:19 Search time 12 seconds

(without alignments) 314,521 Million bits Date 07/05/03

Title: us-09-646-651a.1

Perfect score: 471 1 EEDLEHRLINIHHSVTE.....HVEVLYEVLAMNNHRE 91

Sequence: 1 EEDLEHRLINIHHSVTE.....HVEVLYEVLAMNNHRE 91

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Result No. Score Match Length DB ID

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Summary

Description

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3 420 67.9 91 1 S112_HUMAN

4 264 67.9 81 1 S112_PIG

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12 160 34.0 92 1 S101_PIG

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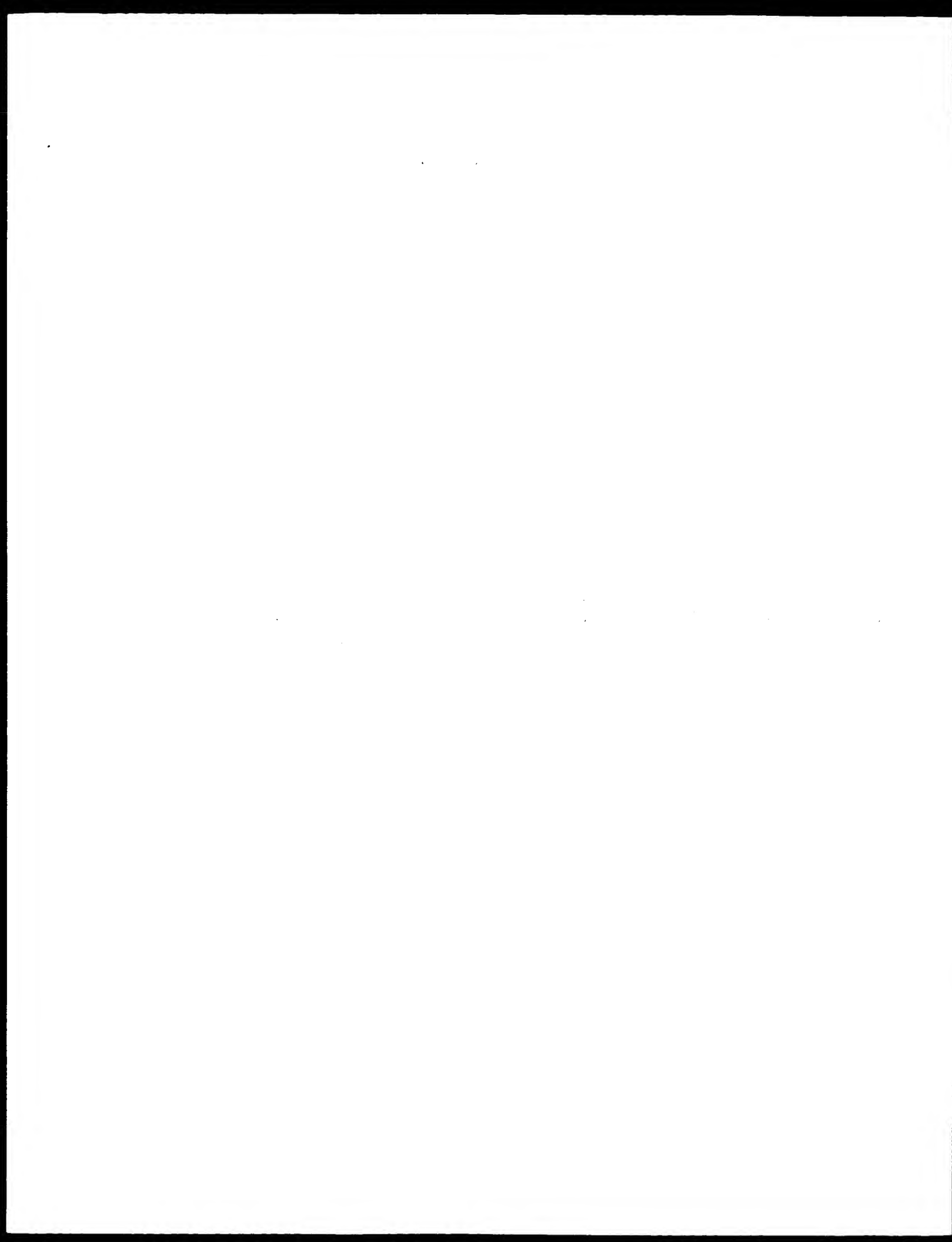
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 FI CA_BIND 53 64 EF_HAND 2 (HIGH AFFINITY) (POTENTIAL)
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 DT 01-JAN-1983 (Feb. 96, Created)
 DT 01-JAN-1988 (Feb. 06, Last sequence update)
 DT 15-JUN-2002 (Feb. 41, Last annotation update)
 DE Calgranulin B (Calcium-binding protein B)
 DE (MBP-14) (F11) (terkoyto, Li complex heavy chain) (S100
 DE binding protein B9) (Calprotectin B9 subunit).
 DE S100A9 or MBP-4 or CAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RA Ojink K., Corlelli N., Brington J., Clerc F.G., Larsson L., Wallis G.,
 RA Gerhards G., Schlegel P., Sorg G.;
 RA "Two calcium-binding proteins in infiltrate macrophages of human
 RA arthritis."
 RT Arthritis.
 RT NATURE 340:80-82(1993);
 RN 12;
 RP SEQUENCE FROM N.A.
 RX MEDLINE:8830148; PubMed:3405210;
 RA Lagasse F., Clerc F.G.;
 RA "Cloning and expression of two human genes encoding calcium-binding
 RA proteins that are regulated during myeloid differentiation."
 RT Mol. Cell. Biol. 8:2402-2410(1988).
 RN 13;
 RP SEQUENCE FROM N.A.
 RX MEDLINE:8925276; PubMed:2656677;
 RA Murao S., Collier F.R., Huberman F.;
 RA "A protein containing the cystic fibrosis antigen is an inhibitor of
 RA protein kinases."
 RT J. Biol. Chem. 264:8356-8360(1989).
 RN 14;
 RP SEQUENCE FROM N.A. AND VARIANT AFG 20.
 RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
 RA "Human gene for migration inhibitory factor-related protein 14
 RA (MIRP14), contains alleles."
 RT Submitted (FEF-2000) to the EMBL/GenBank/DBS1 databases.
 RN 15;
 RP SEQUENCE OF 84-114, AND PHOSPHORYLATION.
 RX MEDLINE:90044076; PubMed:2478891;
 RA Edgworth J., Freeman P., Hoag N.;
 RA "Tomographic analysis of phospho-epitopes on the myeloid antigen B122
 RA protein p14.";
 RL Nature 442:189-192(1998).
 RN 16;
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 EX MEDLINE:941041; PubMed:1286667;
 RA Kasmussen H.H., Van Damme J., Puype M., Gesser B., Colls J.E.,
 RA Vanderkerckhove J.;
 RA "Microsequences of 145 proteins recorded in the two-dimensional gel
 RA protein database of normal human epidermal keratinocytes."
 RT Electrophoresis 13:960-969(1992).
 RN 17;
 RP SEQUENCE OF 5-34.
 EX MEDLINE:9219334; PubMed:8422249;
 RA Miyasaki K.T., Rodan A.L., Marthy A.R., Leber R.L.;
 RA "In vitro antimicrobial activity of the human neutrophil cytosolic S-
 RA 100 protein complex, calprotectin, against *Candida albicans* spores."
 RT J. Dent. Res. 72:517-523(1993).
 DE ENLICH, INDICATED BY NAME HUBER IS ACTIVITY OF AMYLOSE TISSUES
 DE AND IN CHRONIC INFLAMMATIONS, SEEM TO BE AN INDICATOR OF PROTEIN
 DE KINASES, ALSO EXRESSED IN EPITHELIAL CELLS CONSTITUTIVELY OR
 DE INDUCED DURING DYSPLASIS, MAY INTERACT WITH COMPONENTS OF THE
 DE INTRACELLULAR FILAMENTARY CYTOSKELETON AND WITH EPITHELIAL CELLS.
 DE -1- MISCELLANEOUS: HAS BEEN SHOWN TO BIND CALCIUM.
 DE -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DE -1- SIMILARITY: COMPARES 2 EF HAND CALCIUM BINDING SITES
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 EMBL: AF237964; AAF62929.1;
 EMBL: AF237965; AAF62930.1;
 EMBL: AF237

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF HAND CATION BINDING DOMAINS.
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 DR EMBL: M4318; AA07229.1;
 DR EMBL: S57123; AA025840.1;
 DR EMBL: X87966; CAA61204.1;
 DR PIR: A42488; A12488.
 DR HSP: P05109; IRR8.
 DR MG: MG18834; C1702.
 DR InterPro: IPR001751; GABP_S100.
 DR InterPro: IPR02048; EF-hand.
 DR Pfam: PF00046; EF-hand_1.
 DR Pfam: PF01023; S_100_1.
 DR Prodom: P000407; GABP_S100_1.
 DR ProSITE: PS00018; EF_HAND_1.
 DR ProSITE: PS00433; S100_CAMP_1.
 KW Calcium-binding; Chemotaxis.
 FT INIT_MET 0
 FT CALBIND 19 42 EF HAND 1 (LOW AFFINITY) (FUNCTIONAL).
 FT CALBIND 58 69 EF HAND 2 (HIGH AFFINITY) (FUNCTIONAL).
 FT CONFLICT 56 66 E -> D (1N REF. 1).
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 DB 2 SELEKALSTLIVNYNSHIOGHIALYKNDPKKVVTEDEYQVQNT NITLITFL 57
 QY 61 DANQGVGVKFEVAVLVTVITLADNIIKE 91
 DB 58 DVNSDAIVETETIVLVVAHRSIHE 88
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 AC P50115;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
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 DE (P8).
 GN S100A8 or MRP9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: Lewis/34; Tissue: testicular ovary;
 RA MEDLINE: 94343442; PubMed: 8343166;
 RA Imachi T., Uchida I., Wahl S.M., McGarity-Francis N.;
 RT "Expression and cloning of migration inhibitory factor-related
 RT protein (MRP) 8 and MRP14 in arthritis-susceptible rats.";
 RL Biochem. Biophys. Res. Commun. 194:819-825(1993).
 RN [2]
 RP SEQUENCE AND ALTYLATION.
 RC Tissue: Spleen;
 RA MEDLINE: 98249881; PubMed: 9570842;
 RA Rattery M.J., Geegzy C.L.;
 RT "Identification of posttranslational modifications and cDNA sequencing
 RT errors in the rat S100 proteins MRP8 and 14 using electrospray

RF Ionization mass spectrometry.";
 RL Acad. Biochem. Sci. 27:271(1998).
 CC -1- FUNCTION: HAS MAXIMAL CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY
 CC PLAY AN IMPOUNTABLE ROLE IN CELLULAR IMMUNE REACTIONS.
 CC -1- SOURCE: HOMOINER AN/HR HETEROINER.
 CC -1- MASS SPECTROMETRY: MW: 1049; MW: 2; METHOD: Electrospray.
 CC -1- BISTANDARD: BINS TWO CATION IONS PER MOLECULE WITH AN
 CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF HAND CATION BINDING DOMAINS.
 CC
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 DR EMBL: J18941; AAA1637.1;
 DR HSP: P05109; IRR8.
 DR InterPro: IPR01751; GABP_S100.
 DR InterPro: IPR02048; EF-hand.
 DR Pfam: PF00046; EF-hand_1.
 DR Pfam: PF01023; S_100_1.
 DR Prodom: P000407; GABP_S100_1.
 DR SWAN: S00054; EFH_1.
 DR ProSITE: PS00018; EF_HAND_1.
 DR ProSITE: PS00433; S100_CAMP_1.
 KW Calcium-binding; Chemotaxis; Acetylation.
 FT INIT_MET 0
 FT CALBIND 19 42 EF HAND 1 (LOW AFFINITY) (FUNCTIONAL).
 FT CALBIND 58 69 EF HAND 2 (HIGH AFFINITY) (FUNCTIONAL).
 FT CONFLICT 72 72 V -> A (1N REF. 1).
 FT SEQUENCE 88 AA; 10153 MW; 2569779A60A03AF CDS; 1;
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 Best Local Similarity 34.1%; Prod. No. 2.7e-09;
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 DB 2 SELEKALSTLIVNYNSHIOGHIALYKNDPKKVVTEDEYQVQNT NITLITFL 57
 QY 61 DANQGVGVKFEVAVLVTVITLADNIIKE 91
 DB 58 DVNSDAIVETETIVLVVAHRSIHE 88

Search completed: May 15, 2003, 11:45:04
 Job time: 12 secs



file	name	format
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D1	(1) NoV [996, (TEMP, r0, ol, t'eatob)]	

161 01 JUN 2002 (TUESDAY), 21. Last annotation update
162 [01JUN, 1.1 (Protocol in 'end') (Placement)].
163 [01JUN, 1.1 (Protocol in 'end') (Placement)].

US Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumetazoa; Platyhelminthes; Cephalopoda; Mollusca; Bivalvia;
 OC NCBT_taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Labeled
 KL Submitted (Oct-2000) to the NCBI GenBank/EMBL/DBPSS
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 DR EMBL: AL356504; CAC13172.1;
 DR HSSP: P80511; 1P8A.
 DR InterPro: IPR001751; CAPR_S100.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR003493; F11aggrin.
 DR Pfam: PF00046; ehand; 1.
 DR Pfam: PF04516; f11aggrin; 3.
 DR Pfam: PF01024; S_100; 1.
 DR PRINTS: PR00447; F11AGGRIN.
 DR SMART: SM00054; EFh; 1.
 DR PROSITE: PS00118; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00404; S100_CAPP; UNPROCN_1.
 FT NINIER 637 687
 FT SEQUENCE 687 AA; 76659 MW; 8000463FFFE077A CPGCA;
 SQ

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 34.8%; Prod. No. 1,28-05;
 Matches 41; Conservative 22; Mismatch 19; Gaps 0

62 ANOGEVSFEKVVVIVVILLAHNIHKE 91
 64 DINKRITTEFLIMPEKLAQVVESTKRE 92

RESULT 10

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 34.8%; Prod. No. 1,28-05;
 Matches 41; Conservative 22; Mismatch 19; Gaps 0

US Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumetazoa; Platyhelminthes; Cephalopoda; Mollusca; Bivalvia;
 OC NCBT_taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Labeled
 KL Submitted (Oct-2000) to the NCBI GenBank/EMBL/DBPSS
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL: AL356504; CAC13172.1;
 DR HSSP: P80511; 1P8A.
 DR InterPro: IPR001751; CAPR_S100.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR003493; F11aggrin.
 DR Pfam: PF00046; ehand; 1.
 DR Pfam: PF04516; f11aggrin; 3.
 DR Pfam: PF01024; S_100; 1.
 DR PRINTS: PR00447; F11AGGRIN.
 DR SMART: SM00054; EFh; 1.
 DR PROSITE: PS00118; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00404; S100_CAPP; UNPROCN_1.
 FT NINIER 637 687
 FT SEQUENCE 687 AA; 76659 MW; 8000463FFFE077A CPGCA;
 SQ

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 32.2%; Prod. No. 1,30-05;
 Matches 29; Conservative 22; Mismatch 7; Gaps 0

62 ANOGEVSFEKVVVIVVILLAHNIHKE 91
 64 DINKRITTEFLIMPEKLAQVVESTKRE 92

RESULT 11

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 34.8%; Prod. No. 1,28-05;
 Matches 41; Conservative 22; Mismatch 19; Gaps 0

US Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumetazoa; Platyhelminthes; Cephalopoda; Mollusca; Bivalvia;
 OC NCBT_taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Labeled
 KL Submitted (Oct-2000) to the NCBI GenBank/EMBL/DBPSS
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL: AL356504; CAC13172.1;
 DR HSSP: P80511; 1P8A.
 DR InterPro: IPR001751; CAPR_S100.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00046; ehand; 1.
 DR Pfam: PF04516; f11aggrin; 3.
 DR Pfam: PF01024; S_100; 1.
 DR PRINTS: PR00447; F11AGGRIN.
 DR SMART: SM00054; EFh; 1.
 DR PROSITE: PS00118; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00404; S100_CAPP; UNPROCN_1.
 FT NINIER 637 687
 FT SEQUENCE 687 AA; 76659 MW; 8000463FFFE077A CPGCA;
 SQ

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 34.8%; Prod. No. 1,30-06;
 Matches 29; Conservative 21; Mismatch 7; Gaps 0

62 ANOGEVSFEKVVVIVVILLAHNIHKE 91
 64 DINKRITTEFLIMPEKLAQVVESTKRE 92

RESULT 12

Query Match 30.5%; Score 144; DB 4; Length 697
 Host Local Similarity 34.8%; Prod. No. 1,30-06;
 Matches 29; Conservative 21; Mismatch 7; Gaps 0

US Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumetazoa; Platyhelminthes; Cephalopoda; Mollusca; Bivalvia;
 OC NCBT_taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Labeled
 KL Submitted (Oct-2000) to the NCBI GenBank/EMBL/DBPSS
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 DR EMBL: AL356504; CAC13172.1;
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 DR Pfam: PF00046; ehand; 1.
 DR Pfam: PF04516; f11aggrin; 3.
 DR Pfam: PF01024; S_100; 1.
 DR PRINTS: PR00447; F11AGGRIN.
 DR SMART: SM00054; EFh; 1.
 DR PROSITE: PS00118; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00404; S100_CAPP; UNPROCN_1.
 FT NINIER 637 687
 FT SEQUENCE 687 AA; 76659 MW; 8000463FFFE077A CPGCA;
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61 (MURK) (FETTERED) (FETTERED)
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61 (MURK) (FETTERED) (FETTERED)
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